

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Tobin, James
- (ii) TITLE OF INVENTION: HUMAN INTERLUEKIN-11 RECEPTOR
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brown, Scott A.
 - (B) REGISTRATION NUMBER: 32,724
 - (C) REFERENCE/DOCKET NUMBER: G15252
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 498-8224
 - (B) TELEFAX: (617) 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 734..1999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCGCCACCC CCAGCCCTCTG GCAGCAGCCA GGGCATCTGG ATCTGCTTAA CTACACAGCC
CCAGCCTGCA CCCTAGCCCC ATCCAGCTTC ACAAACTGGA GACCAACGAA GTGTCAAGAG
CCAGGCCAG CTGAGTGGCC CAAGTAGCCA GACCAAGGAG CCAGGTTCAAG GCGAGAAGCC
TGCGAGCCAG GGCAGGGGTG GGCCTCAGGG TGGGAGTGCA GGATGGGCTC AGATCCATGA
TGACACCCTT CCCCCAGGGT GATAAGGTCT GCCTAGGTTA ATCAGAGGCC GTGATAAGCC
CTGGACCAGG TGGGGTAAA TACCAAAATT CCCAACAGCT GGACTGGAGG GGTTAATGGG
AGTGGCTGAG CTGGTGCAG TGCTTGGTGC CAGGGGGGG CGCCAAGGGC AGTGGAGGG
GAGTTGCTGG CACAGTCTGT TGCCCTCGGGC TTTTGTTCTG GGCCCTAAGC CCAGGACTGA
GATGGGGGT GTGAGGGGT GTGTGTGTCC GTGTGTGTGT GTGCGCGGC
ACGCACATGC AAAGCACTGG GTATACAGTG GGAAAGGGGA CCTCAGGTCA GTTCCCGCAG
60
120
180
240
300
360
420
480
540
600

TGATTTCTAA CAGCCTTACCCACTGGTG CATCAATTTC TCTCCTAGGA AGCCTCAGTT 660
 TTGGAGAGGA AGAGCCAGGC TTAGCCTCC CATCTCAGGG GTGGGGATT TTGACTTA
 CCTCTCCCCA CAG ATG AGC AGC TGC TCA GGG CTG AGC AGG GTC CTG 720
 Met Ser Ser Cys Ser Gly Leu Ser Arg Val Leu
 1 5
 15
 GTG GCC GTG GCT ACA GCC CTC GTG TCT GCC TCC TCC CCC TGC CCC CAG 769
 Val Ala Val Ala Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln
 20
 25
 GCC TGG GGC CCC CCA GGG GTC CAG TAT GGG CAG CCA GGC AGG TCC GTG 817
 Ala Trp Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val
 30
 35
 AAG CTG TGT TGT CCT GGA GTG ACT GCC GGG GAC CCA GTG TCC TGG TTT 865
 Lys Leu Cys Cys Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe
 45
 50
 CGG GAT GGG GAG CCA AAG CTC CAG GGA CCT GAC TCT GGG CTA GGG 913
 Arg Asp Gly Glu Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly
 65
 70
 CAT GAA CTG GTC CTG GCC CAG GCA GAC AGC ACT GAT GAG GGG ACC TAC 961
 His Glu Leu Val Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr
 80
 85
 ATC TGC CAG ACC CTG GAT GGT GCA CTT GGG GGC ACA GTG ACC CTG CAG 1009
 Ile Cys Gln Thr Leu Asp Gly Ala Leu Gly Thr Val Thr Leu Gln
 95
 100
 CTG GGC TAC CCT CCA GCC CGC CCT GTT GTC TCC TGC CAA GCA GCC GAC 1057
 Leu Gly Tyr Pro Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp
 110
 115
 TAT GAG AAC TTC TCT TGC ACT TGG AGT CCC AGC CAG ATC AGC GGT TTA 1105
 Tyr Glu Asn Phe Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu
 125
 130
 135
 140

የኢትዮጵያ ዘመንና ስምምነት

CCC ACC CGC TAC CTC ACC TCC TAC AGG AAG ACA GTC CTA CGA GCT		1201
Pro Thr Arg Tyr Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala	145	155
GAT AGC CAG AGG AGG AGT CCA TCC ACA GGG CCC TGG CCA TGC CCA CAG		1249
Asp Ser Gln Arg Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln	160	165
GAT CCC CTA GGG GCT GCC CGC TGT GTC CAC GGG GCT GAG RTC TGG		1297
Asp Pro Leu Gly Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp	175	180
AGC CAG TAC CGG ATT AAT GTG ACT GAG GTG AAC CCA CTG GGT GCC AGC		1345
Ser Gln Tyr Arg Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser	190	195
ACA CGC CTG CTG GAT GTG AGC TTG CAG AGC ATC TTG CGC CCT GAC CCA		1393
Thr Arg Leu Leu Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro	205	210
CCC CAG GGC CTG CGG GTA GAG TCA GTA CCA GGT TAC CCC CGA CGC CTG		1441
Pro Gln Gly Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu	225	230
CGA GCC AGC TGG ACA TAC CCT GCC TCC TGG CCG TGC CAG CCC CAC TTC		1489
Arg Ala Ser Trp Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe	240	245
CTG CTC AAG TTC CGT TTG CAG TAC CGT CCG GCG CAG CAT CCA GCC TGG		1537
Leu Leu Lys Phe Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp	255	260
TCC ACG GTG GAG CCA GCT GGA CTG GAG GAG GTG ATC ACA GAT GCT GTG		1585
Ser Thr Val Glu Pro Ala Gly Leu Gln Glu Val Ile Thr Asp Ala Val	270	275
GCT GGG CTG CCC CAT GCT GTA CGA GTC AGT GCC CGG GAC TTT CTA GAT		1633
Ala Gly Leu Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp	285	290
		300

CATGTGCTG TGAGGCAGGG AACATGTATT CTCTGCATGC ATGTATGTAG GTGCCTGGGG 2319
AGTGTGCTG GGTCCTTGGC TCTTGGCTT TCCCCTTNGCA GGGGTGTGC AGGTGTGAAT 2379
AAAGAGAATA AGGAAGTCT TGGAGATTAT ACTCAGAAAA AAAAAGAAA AGTCGACGCG 2439
GCCGGAATT CCTGCAG 2456

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ser Ser Cys Ser Gly Leu Ser Arg Val Leu Val Ala Val Ala
1 5 10 15
Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro
20 25 30
Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val Lys Leu Cys Cys
35 40 45
Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe Arg Asp Gly Glu
50 55 60
Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Glu Leu Val
65 70 75 80
Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr Ile Cys Gln Thr
85 90 95
Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln Leu Gly Tyr Pro
100 105 110

Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp Tyr Glu Asn Phe
 115 120 125
 Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu Pro Thr Arg Tyr
 130 135 140
 Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala Asp Ser Gln Arg
 145 150 155 160
 Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Gly
 165 170 175
 Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Gln Tyr Arg
 180 185 190
 Ile Asn Val Thr Glu Val Val Asn Pro Leu Gly Ala Ser Thr Arg Leu Leu
 195 200 205
 Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu
 210 215 220
 Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu Arg Ala Ser Trp
 225 230 235 240
 Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu Leu Lys Phe
 245 250 255
 Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu
 260 265 270
 Pro Ala Gly Leu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro
 275 280 285
 His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp
 290 295 300
 Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Thr Ile
 305 310 315 320
 Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr Gln Pro Glu Val

325	330	335	
Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro Ser Leu Gln Pro			
340	345	350	
His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu Gln Val Ala Val			
355	360	365	
Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu Val Ala Gly Ala			
370	375	380	
Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Gly Lys Asp Gly			
385	390	395	400
Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro Val Asp Arg Arg			
405	410	415	
Pro Gly Ala Pro Asn Leu			
420			

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1714 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 34..1359

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTCTTAGCCT	GATAGGAGGA	AGTCTTGAG	GCC ATG GCA CTC AGT CAC TGT GAT	54
TAT CAA GAT GAG CAG CAG CTG CTC AGG GCT GAC CAG GGT CCT CGT GGC	Met Ala Leu Ser His Cys Asp			
Tyr Gln Asp Glu Gln Gln Leu Leu Arg Ala Asp Gln Gly Pro Gly Gly				
10	15	20	25	30
CGT GCT ACA GCC CTG GTG TCT TCC TCC CCC TGC CCC CAA GCT TGG	102	150		
Arg Ala Thr Ala Leu Val Ser Ser Ser Pro Cys Pro Gln Ala Trp				
25	30	35		
GGT CCT CCA GGG GTC CAG TAT GGA CAA CCT GGC AGG CCC GTG ATG CTG	198			
Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Pro Val Met Leu				
40	45	50	55	
TGC TGC CCC GGA GTG AGT GCT GGG ACT CCA GTG TCC TGG TTT CGG GAT	246			
Cys Cys Pro Gly Val Ser Ala Gly Thr Pro Val Ser Trp Phe Arg Asp				
60	65	70		
GGA GAT TCA AGG CTG CTC CAG GGA CCT GAC TCT GGG TTA GGA CAC AGA	294			
Gly Asp Ser Arg Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Arg				
75	80	85		
CTG GTC TTG GCC CAG GTG GAC AGC CCT GAT GAA GGC ACT TAT GTC TGC	342			
Leu Val Leu Ala Gln Val Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys				
90	95	100		
CAG ACC CTG GAT GGT GTA TCA GGG GGC ATG GTG ACC CTG AAG CTG CGC	390			
Gln Thr Leu Asp Gly Val Ser Gly Gln Met Val Thr Leu Lys Leu Gly				
105	110	115		
TTT CCC CCA GCA CGT CCT GAA GTC TCC TGC CAA GCG GTA GAC TAT GAA	438			
Phe Pro Pro Ala Arg Pro Glu Val Ser Cys Gln Ala Val Asp Tyr Glu				
120	125	130	135	
AAC TTC TCC TGT ACT TGG AGT CCA GGC CAG GTC AGC GGT TTG CCC ACC	486			
Asn Phe Ser Cys Thr Trp Ser Pro Gly Gln Val Ser Gly Leu Pro Thr				
140	145	150		

CGC TAC CTT ACT TCC TAC AGG AAG AAG	ACG CTG CCA GGA GCT GAG AGT	534
Arg Tyr Leu Thr Ser Tyr Arg Lys Lys	Thr Leu Pro Gly Ala Glu Ser	
155	160	165
CAG AGG GAA AGT CCA TCC ACC GGG CCT	TGG CCG TGT CCA CAG GAC CCT	582
Gln Arg Glu Ser Pro Ser Thr Gly Pro	Trp Pro Cys Pro Gln Asp Pro	
170	175	180
CTG GAG GCC TCC CGA TGT GTG GTC CAT	GGG GCA GAG TTC TGG AGT GAG	630
Leu Glu Ala Ser Arg Cys Val Val His	Gly Ala Glu Phe Trp Ser Glu	
185	190	195
TAC CGG ATC AAT GTG ACC GAG GTG AAC	CCA CTG GGT GCC AGC ACG TGC	678
Tyr Arg Ile Asn Val Thr Glu Val Asn	Pro Leu Gly Ala Ser Thr Cys	
200	205	210
CTA CTG GAT GTG AGA TTA CAG AGC ATC	TTC CGT CCT GAT CCA CCC CAA	726
Leu Leu Asp Val Arg Leu Gln Ser Ile	Leu Arg Pro Asp Pro Gln	
220	225	230
GGA CTG CGG GTG GAA TCC GTA CCT GGT	TAC CCG AGA CGC CTG CAT GCC	774
Gly Leu Arg Val Glu Ser Val Pro Gly	Tyr Pro Arg Arg Leu His Ala	
235	240	245
AGC TGG ACA TAC CCT GCC TCC TGG CGT	CGC CAA CCC CAC TTT CTG CTC	822
Ser Trp Thr Tyr Pro Ala Ser Trp Arg Arg	Gln Pro His Phe Leu Leu	
250	255	260
AAG TTG CGG TTG CAA TAC CGA CCA GCA	CAG CAT CCA GCC TGG TCC ACG	870
Lys Phe Arg Leu Gln Tyr Arg Pro Ala	Gln His Pro Ala Trp Ser Thr	
265	270	275
GTG GAG CCC ATT GGC TTG GAG GAA	GTG ATA ACA GAT GCT GTG GCT	918
Val Glu Pro Ile Gly Leu Glu Val Ile	Thr Asp Ala Val Ala Gly	
280	285	290
CTG CCA CAC GCG GTC CGA GTC AGT	GCC AGG GAC TTT CTG GAT GCT	966
Leu Pro His Ala Val Arg Val Ser Ala	Arg Asp Phe Leu Asp Ala Gly	
300	305	310

“கால்களை விடுவதே நீண்ட பால்”

ACC TGG AGC GCC TGG AGC CCA GAG GCC TGG GGT ACT CCT AGC ACT GGT		1014
Thr Trp Ser Ala Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly	315	320
CCC CTG CAG GAT GAG ATA CCT GAT TGG AGC CAG GGA CAT GGA CAG CAG		1062
Pro Leu Gln Asp Glu Ile Pro Asp Trp Ser Gln Gly His Gly Gln Gln	330	335
CTA GAG GCA GTA GTA GCT CAG GAG GAC AGC CCG GCT CCT GCA AGG CCT		1110
Leu Glu Ala Val Ala Gln Glu Asp Ser Pro Ala Pro Ala Arg Pro	345	350
TCC TTG CAG CCG GAC CCA AGG CCA CTT GAT CAC AGG GAC CCC TTG GAG		1158
Ser Leu Gln Pro Asp Pro Arg Pro Leu Asp His Arg Asp Pro Leu Glu	360	365
CAA GTA GCT GTG TTA GCG TCT CTG GGA ATC TTC TCT TGC CTT GGC CTG		1206
Gln Val Ala Val Leu Ala Ser Leu Gly Ile Phe Ser Cys Leu Gly Leu	380	385
GCT GTT GGA GCT CTG GCA CTG GGG CTC TGG CTG AGG CTG AGA CGG AGT		1254
Ala Val Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Ser	395	400
GGG AAG GAT GGA CCG CAA AAA CCT GGG CTC TTG GCA CCC ATG ATC CCG		1302
Gly Lys Asp Gly Pro Gln Lys Pro Gly Leu Leu Ala Pro Met Ile Pro	410	415
GTG GAA AAG CTT CCA GGA ATT CCA AAC CTC CAG AGG ACC CCA GAG AAC		1350
Val Glu Lys Leu Pro Gly Ile Pro Asn Leu Gln Arg Thr Pro Glu Asn	425	430
TTC AGC TGATTTCATC TGTAAACCCGG TCAGACTTGG GGTGGTTAAA AGGACAGGCA		1406
Phe Ser	440	
GAAAGGGCG GGGCAGTGGAA TCCCTGTGGAA TGGAGGTCTC AGCTGAAAGT CTGAGCTCTT		1466
TTCCTTGACA CCTATACTCC AAACTTGCTG CGGGCTGAAG GCTGTCTGGAA CTTCCGATGT		1526

CCTGAGGTGG AAGTCCACCT GAGGAATGTG TACAGAAGTC TGTGTTCTG TGATCGTGG 1586
TGATGTGAG ACAGGGGCC AAAGTTCTCT GCATGTGTGT ACAGGTGATT GGAGAGTGG 1646
TGCGGTCTTG GGCTTGGCCC TTCTGGAAAG TGTGAAGACT TGAATAAAA GAGACGGAAAG 1706
TTTTTGGA 1714

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Leu Ser His Cys Asp Tyr Gln Asp Glu Gln Gln Leu Leu Arg
1 5 10 15
Ala Asp Gln Gly Pro Gly Arg Ala Thr Ala Leu Val Ser Ser Ser
20 25 30
Ser Pro Cys Pro Gln Ala Trp Gly Pro Pro Gly Val Gln Tyr Gly Gln
35 40 45
Pro Gly Arg Pro Val Met Leu Cys Cys Pro Gly Val Ser Ala Gly Thr
50 55 60
Pro Val Ser Trp Phe Arg Asp Gly Asp Ser Arg Leu Leu Gln Gly Pro
65 70 75 80
Asp Ser Gly Leu Gly His Arg Leu Val Ala Gln Val Asp Ser Pro
85 90 95
Asp Glu Gly Thr Tyr Val Cys Gln Thr Leu Asp Gly Val Ser Gly Gly
100 105 110

Met	Val	Thr	Leu	Lys	Leu	Gly	Phe	Pro	Ala	Arg	Pro	Glu	Val	Ser	
115			120												
Cys	Gln	Ala	Val	Asp	Tyr	Glu	Asn	Phe	Ser	Cys	Thr	Trp	Ser	Pro	Gly
130			135												140
Gln	Val	Ser	Gly	Leu	Pro	Thr	Arg	Tyr	Leu	Thr	Ser	Tyr	Arg	Lys	Lys
145			150												155
Thr	Leu	Pro	Gly	Ala	Glu	Ser	Gln	Arg	Glu	Ser	Pro	Ser	Thr	Gly	Pro
			165												170
Trp	Pro	Cys	Pro	Gln	Asp	Pro	Leu	Glu	Ala	Ser	Arg	Cys	Val	Val	His
			180												185
Gly	Ala	Glu	Phe	Trp	Ser	Glu	Tyr	Arg	Ile	Asn	Val	Thr	Glu	Val	Asn
			195												200
Pro	Leu	Gly	Ala	Ser	Thr	Cys	Leu	Leu	Asp	Val	Arg	Leu	Gln	Ser	Ile
			210												215
Leu	Arg	Pro	Asp	Pro	Pro	Gln	Gly	Leu	Arg	Val	Glu	Ser	Val	Pro	Gly
			225												230
Tyr	Pro	Arg	Arg	Leu	His	Ala	Ser	Trp	Thr	Tyr	Pro	Ala	Ser	Trp	Arg
			245												250
Arg	Gln	Pro	His	Phe	Leu	Leu	Lys	Phe	Arg	Leu	Gln	Tyr	Arg	Pro	Ala
			260												265
Gln	His	Pro	Ala	Trp	Ser	Thr	Val	Glu	Pro	Ile	Gly	Leu	Glu	Glu	Val
			275												280
Ile	Thr	Asp	Ala	Val	Ala	Gly	Leu	Pro	His	Ala	Val	Arg	Val	Ser	Ala
			290												295
Arg	Asp	Phe	Leu	Asp	Ala	Gly	Thr	Trp	Ser	Ala	Trp	Ser	Pro	Glu	Ala
			305												310
Trp	Gly	Thr	Pro	Ser	Thr	Gly	Pro	Leu	Gln	Asp	Glu	Ile	Pro	Asp	Trp

Ser Gln Gly His Gly Gln Gln Leu Glu Ala Val Val Ala Gln Glu Asp	325	330	335
340	345	350	355
Ser Pro Ala Pro Ala Arg Pro Ser Leu Gln Pro Asp Pro Arg Pro Leu	355	360	365
Asp His Arg Asp Pro Leu Glu Gln Val Ala Val Leu Ala Ser Leu Gly	370	375	380
Ile Phe Ser Cys Ile Gly Leu Ala Val Gly Ala Leu Gly Leu	385	390	395
Trp Leu Arg Leu Arg Arg Ser Gly Lys Asp Gly Pro Gln Lys Pro Gly	405	410	415
Leu Leu Ala Pro Met Ile Pro Val Glu Lys Leu Pro Gly Ile Pro Asn	420	425	430
Leu Gln Arg Thr Pro Glu Asn Phe Ser	435	440	445

GCT GGC ACC TGG AGC ACC TGG AGC CCG GAG GCC TGG GGA ACT CCG AGC Ala Gly Thr Trp Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser	1681 305
ACT GGG ACC ATA CCA AAG GAG ATA CCA GCA TGG GGC CAG CTA CAC ACG Thr Gly Thr Ile Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr	1729 320
CAG CCA GAG GTG GAG CCT CAG GTG GAC AGC CCT GCT CCA AGG CCC Gln Pro Glu Val Glu Pro Gln Val Asp Ser Pro Ala Pro Arg Pro	1777 325
TCC CTC CAA CCA CAC CCT CGG CTA CTT GAT CAC AGG GAC TCT GTG GAG Ser Leu Gln Pro His Pro Arg Leu Asp His Arg Asp Ser Val Glu	1825 345
CAG GTA GCT GTG CTG GCG TCT TTG GGA ATC CTT TCT TTC CTG GGA CTG Gln Val Ala Val Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu	1873 350
GTC GCT GGG GCC CTG GCA CTG GGG CTC TGG CTG AGG CTG AGA CGG GGT Val Ala Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Gly	1921 365
GGG AAG GAT GGA TCC CCA AAG CCT GGG TTC TGT GCC TCA GTG ATT CCA Gly Lys Asp Gly Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro	1969 370
GTG GAC AGG CGT CCA GGA GCT CCA AAC CTG TAGAGGCC AGGAGGCTT Val Asp Arg Arg Pro Gly Ala Pro Asn Leu	2019 385
CGGGAGATT CACCTATAAT TCTCTCTTGC TGGTGTGGAT GGATGGACAG ATAGAAACCA GGCAGGACAG TAGATCCCTA TGGTTGGATC TCAGCTGGAA GTTCTGTTG GAGCCCCATT	2079 390
CTGTGAGACC CTGTATTCA AATTGCAGC TGAAAGGTGC TTGTACCTCT GATTTCACCC CAGAGTTGGA GTTCTGCTCA AGGAACGTGT GTAATGTGTA CATCTGTGTC CATGTGTGAC	2139 405
	2199 420
	2259